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9 leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or
10 45 of JS *cp45*, and/or a mutation in an N gene start sequence at a position corresponding to
11 nucleotide 62 of JS *cp45*, said genome or antigenome] combined with one or more
12 heterologous gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of
13 HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV genome or
14 antigenome.

1 21. (Twice Amended) The chimeric PIV of claim [6] 1, wherein the
2 chimeric genome or antigenome incorporates at least one and up to a full complement of
3 attenuating mutations present within HPIV3 JS *cp45*.

C2
1 22. (Twice Amended) The chimeric PIV of claim [6] 1, wherein the
2 chimeric genome or antigenome incorporates at least one and up to a full complement of
3 attenuating mutations specifying an amino acid substitution in the L protein at a position
4 corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of in JS *cp45*; in the N protein at a position
5 corresponding to residues Val₉₆ or Ser₃₈₉ of JS *cp45*, in the C protein at a position
6 corresponding to Ile₉₆ of JS *cp45*, in the F protein at a position corresponding to residues Ile₄₂₀
7 or Ala₄₅₀ of JS *cp45*, in the HN protein at a position corresponding to residue Val₃₈₄ of JS *cp45*,
8 a nucleotide substitution in a 3' leader sequence of the chimeric virus at a position
9 corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a mutation in an N gene start
10 sequence at a position corresponding to nucleotide 62 of JS *cp45*.

C3
1 39. (Twice Amended) An isolated polynucleotide comprising a chimeric
2 parainfluenza virus (PIV) genome or antigenome which includes a partial or complete human
3 parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at least
4 one and up to a full complement of attenuating mutations present within HPIV3 JS *cp45*
5 selected from mutations specifying an amino acid substitution in the L protein at a position
6 corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS *cp45*; in the N protein at a position
7 corresponding to residues Val₉₆ or Ser₃₈₉ of JS *cp45*, in the C protein at a position
8 corresponding to Ile₉₆ of JS *cp45*, a nucleotide substitution in a 3' leader sequence of the
9 chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a
10 mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp45*,

C3 11 said genome or antigenome] combined with one or more heterologous gene(s) or genome
12 segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of
13 one or both of HPIV1 and HPIV2 to form a chimeric PIV genome or antigenome.

1 48. (Twice Amended) A method for producing an infectious attenuated
2 chimeric parainfluenza virus (PIV) particle from one or more isolated polynucleotide
3 molecules encoding said PIV, comprising:

C4 4 expressing in a cell or cell-free lysate an expression vector comprising an
5 isolated polynucleotide comprising a partial or complete human parainfluenza virus 3 JS
6 (HPIV3 JS) vector genome or antigenome [that incorporates at least one and up to a full
7 complement of attenuating mutations present within HPIV3 JS *cp45* selected from mutations
8 specifying an amino acid substitution in the L protein at a position corresponding to Tyr₉₄₂,
9 Leu₉₉₂, or Thr₁₅₅₈ of JS *cp45*; in the N protein at a position corresponding to residues Val₉₆ or
10 Ser₃₈₉ of JS *cp45*, in the C protein at a position corresponding to Ile₉₆ of JS *cp45*, a nucleotide
11 substitution in a 3' leader sequence of the chimeric virus at a position corresponding to
12 nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a mutation in an N gene start sequence at a
13 position corresponding to nucleotide 62 of JS *cp45*, said genome or antigenome] combined
14 with one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic
15 determinant(s) of HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV
16 genome or antigenome, and PIV N, P, and L proteins.

C5 1 50. (Twice Amended) An expression vector comprising an operably linked
2 transcriptional promoter, a polynucleotide sequence which includes a partial or complete
3 human parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome [that incorporates at
4 least one and up to a full complement of attenuating mutations present within HPIV3 JS *cp45*
5 selected from mutations specifying an amino acid substitution in the L protein at a position
6 corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS *cp45*; in the N protein at a position
7 corresponding to residues Val₉₆ or Ser₃₈₉ of JS *cp45*, in the C protein at a position
8 corresponding to Ile₉₆ of JS *cp45*, a nucleotide substitution in a 3' leader sequence of the
9 chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*, and/or a
10 mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS *cp45*,

05 11 said genome or antigenome] combined with one or more heterologous gene(s) or genome
12 segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of
13 HPIV1 and/or HPIV2 to form a chimeric PIV genome or antigenome, and a transcriptional
14 terminator.

Please add new claims 51-52 as follows:

06 1 --51. The chimeric PIV of claim 6, wherein the chimeric genome or
2 antigenome incorporates at least one and up to a full complement of attenuating mutations
3 present within HPIV3 JS *cp45* selected from mutations specifying an amino acid substitution
4 in the L protein at a position corresponding to Tyr942, Leu992, or Thr1558 of JS *cp45*; in the
5 N protein at a position corresponding to residues Val96 or Ser389 of JS *cp45*, in the C protein
6 at a position corresponding to Ile96 of JS *cp45*, a nucleotide substitution in a 3' leader sequence
7 of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp45*,
8 and/or a mutation in an N gene start sequence at a position corresponding to nucleotide 62 of
9 JS *cp45*.

1 52. The isolated polynucleotide of claim 39, wherein the chimeric genome
2 or antigenome incorporates at least one and up to a full complement of attenuating mutations
3 present within HPIV3 JS *cp45*--